

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/564,665
Source: TEWP
Date Processed by STIC: 1-30-06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 01/30/2006

PATENT APPLICATION: US/10/564,665

TIME: 15:48:49

Input Set : A:\14875-155US1.txt

Output Set: N:\CRF4\01302006\J564665.raw

3 <110> APPLICANT: Irei, Reiko
 4 Tsunoda, Hiroyuki
 5 Igawa, Tomoyuki
 6 Sekimori, Yasuo
 7 Tsuchiya, Masayuki
 9 <120> TITLE OF INVENTION: IgM PRODUCTION BY TRANSFORMED CELL AND
 10 METHOD OF QUANTIFYING THE SAME
 12 <130> FILE REFERENCE: 14875-155US1
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/564,665
 C--> 14 <141> CURRENT FILING DATE: 2006-01-13
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/010444
 15 <151> PRIOR FILING DATE: 2004-07-15
 17 <150> PRIOR APPLICATION NUMBER: US 60/487,333
 18 <151> PRIOR FILING DATE: 2003-07-15
 20 <160> NUMBER OF SEQ ID NOS: 31
 22 <170> SOFTWARE: PatentIn version 3.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1779
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(1779)
 34 <400> SEQUENCE: 1
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 37 1 5 10 15
 39 gtc cag tgt gag gtg cag ctg ttg gat tct ggg gga ggc ttg gta cag 96
 40 Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln
 41 20 25 30
 43 cct ggg ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 144
 44 Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 45 35 40 45
 47 agc agc tgt gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg 192
 48 Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 49 50 55 60
 51 gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca 240
 52 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
 53 65 70 75 80
 55 gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aaa tcc aag aac 288
 56 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
 57 85 90 95
 59 acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta 336

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60	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	
61				100					105					110			
63	tat	tac	tgt	gcg	aaa	ggt	ggc	aac	gat	att	ttg	act	ggt	tat	tat	gct	384
64	Tyr	Tyr	Cys	Ala	Lys	Gly	Gly	Asn	Asp	Ile	Leu	Thr	Gly	Tyr	Tyr	Ala	
65				115					120					125			
67	tgg	ggc	cag	gga	acc	ctg	gtc	acc	gtc	tcc	tca	ggg	agt	gca	tcc	gcc	432
68	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Ser	Ala	Ser	Ala	
69				130					135					140			
71	cca	acc	ctt	ttc	ccc	ctc	gtc	tcc	tgt	gag	aat	tcc	ccg	tcg	gat	acg	480
72	Pro	Thr	Leu	Phe	Pro	Leu	Val	Ser	Cys	Glu	Asn	Ser	Pro	Ser	Asp	Thr	
73	145					150					155					160	
75	agc	agc	gtg	gcc	gtt	ggc	tgc	ctc	gca	cag	gac	ttc	ctt	ccc	gac	tcc	528
76	Ser	Ser	Val	Ala	Val	Gly	Cys	Leu	Ala	Gln	Asp	Phe	Leu	Pro	Asp	Ser	
77				165					170					175			
79	atc	act	ttc	tcc	tgg	aaa	tac	aag	aac	aac	tct	gac	atc	agc	agc	acc	576
80	Ile	Thr	Phe	Ser	Trp	Lys	Tyr	Lys	Asn	Asn	Ser	Asp	Ile	Ser	Ser	Thr	
81				180					185					190			
83	cgg	ggc	ttc	cca	tca	gtc	ctg	aga	ggg	ggc	aag	tac	gca	gcc	acc	tca	624
84	Arg	Gly	Phe	Pro	Ser	Val	Leu	Arg	Gly	Gly	Lys	Tyr	Ala	Ala	Thr	Ser	
85				195					200					205			
87	cag	gtg	ctg	ctg	cct	tcc	aag	gac	gtc	atg	cag	ggc	aca	gac	gaa	cac	672
88	Gln	Val	Leu	Leu	Pro	Ser	Lys	Asp	Val	Met	Gln	Gly	Thr	Asp	Glu	His	
89				210					215					220			
91	gtg	gtg	tgc	aaa	gtc	cag	cac	ccc	aac	ggc	aac	aaa	gaa	aag	aac	gtg	720
92	Val	Val	Cys	Lys	Val	Gln	His	Pro	Asn	Gly	Asn	Lys	Glu	Lys	Asn	Val	
93	225					230					235				240		
95	cct	ctt	cca	gtg	att	gct	gag	ctg	cct	ccc	aaa	gtg	agc	gtc	ttc	gtc	768
96	Pro	Leu	Pro	Val	Ile	Ala	Glu	Leu	Pro	Pro	Lys	Val	Ser	Val	Phe	Val	
97				245						250				255			
99	cca	ccc	cgc	gac	ggc	ttc	ttc	ggc	aac	ccc	cgc	aag	tcc	aag	ctc	atc	816
100	Pro	Pro	Arg	Asp	Gly	Phe	Phe	Gly	Asn	Pro	Arg	Lys	Ser	Lys	Leu	Ile	
101				260					265					270			
103	tgc	cag	gcc	acg	ggt	ttc	agt	ccc	cgg	cag	att	cag	gtg	tcc	tgg	ctg	864
104	Cys	Gln	Ala	Thr	Gly	Phe	Ser	Pro	Arg	Gln	Ile	Gln	Val	Ser	Trp	Leu	
105				275					280					285			
107	cgc	gag	ggg	aag	cag	gtg	ggg	tct	ggc	gtc	acc	acg	gac	cag	gtg	cag	912
108	Arg	Glu	Gly	Lys	Gln	Val	Gly	Ser	Gly	Val	Thr	Thr	Asp	Gln	Val	Gln	
109				290					295					300			
111	gct	gag	gcc	aaa	gag	tct	ggg	ccc	acg	acc	tac	aag	gtg	acc	agc	aca	960
112	Ala	Glu	Ala	Lys	Glu	Ser	Gly	Pro	Thr	Thr	Tyr	Lys	Val	Thr	Ser	Thr	
113	305					310					315				320		
115	ctg	acc	atc	aaa	gag	agc	gac	tgg	ctc	ggc	cag	agc	atg	ttc	acc	tgc	1008
116	Leu	Thr	Ile	Lys	Glu	Ser	Asp	Trp	Leu	Gly	Gln	Ser	Met	Phe	Thr	Cys	
117				325						330				335			
119	cgc	gtg	gat	cac	agg	ggc	ctg	acc	ttc	cag	cag	aat	gcg	tcc	tcc	atg	1056
120	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Gln	Gln	Asn	Ala	Ser	Ser	Met	
121				340					345					350			
123	tgt	gtc	ccc	gat	caa	gac	aca	gcc	atc	cgg	gtc	ttc	gcc	atc	ccc	cca	1104
124	Cys	Val	Pro	Asp	Gln	Asp	Thr	Ala	Ile	Arg	Val	Phe	Ala	Ile	Pro	Pro	

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127 tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg acc tgc ctg      1152
128 Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
129          370          375          380
131 gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc tgg acc cgc      1200
132 Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
133 385          390          395          400
135 cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc gag agc cac      1248
136 Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His
137          405          410          415
139 ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat      1296
140 Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
141          420          425          430
143 gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc cac aca gac      1344
144 Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
145          435          440          445
147 ctg ccc tgc cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc      1392
148 Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala
149          450          455          460
151 ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg      1440
152 Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
153 465          470          475          480
155 aac ctg cgg gag tgc gcc acc atc acg tgc ctg gtg acg ggc ttc tct      1488
156 Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser
157          485          490          495
159 ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc      1536
160 Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
161          500          505          510
163 ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca      1584
164 Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
165          515          520          525
167 ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg      1632
168 Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
169          530          535          540
171 aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc      1680
172 Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
173 545          550          555          560
175 aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc      1728
176 Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
177          565          570          575
179 ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac      1776
180 Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
181          580          585          590
183 tga      1779
185 <210> SEQ ID NO: 2
186 <211> LENGTH: 592
187 <212> TYPE: PRT
188 <213> ORGANISM: Homo sapiens
190 <400> SEQUENCE: 2

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191 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
192 1          5          10          15
194 Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln
195          20          25          30
197 Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
198          35          40          45
200 Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
201          50          55          60
203 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
204 65          70          75          80
206 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
207          85          90          95
209 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
210          100          105          110
212 Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala
213          115          120          125
215 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
216          130          135          140
218 Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
219 145          150          155          160
221 Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
222          165          170          175
224 Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr
225          180          185          190
227 Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser
228          195          200          205
230 Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
231          210          215          220
233 Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
234 225          230          235          240
236 Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
237          245          250          255
239 Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
240          260          265          270
242 Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
243          275          280          285
245 Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
246          290          295          300
248 Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
249 305          310          315          320
251 Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
252          325          330          335
254 Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
255          340          345          350
257 Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
258          355          360          365
260 Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
261          370          375          380
263 Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg

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264 385          390          395          400
266 Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His
267          405          410          415
269 Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
270          420          425          430
272 Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
273          435          440          445
275 Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala
276          450          455          460
278 Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
279 465          470          475          480
281 Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser
282          485          490          495
284 Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
285          500          505          510
287 Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
288          515          520          525
290 Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
291          530          535          540
293 Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
294 545          550          555          560
296 Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
297          565          570          575
299 Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
300          580          585          590
302 <210> SEQ ID NO: 3
303 <211> LENGTH: 723
304 <212> TYPE: DNA
305 <213> ORGANISM: Homo sapiens
307 <220> FEATURE:
308 <221> NAME/KEY: CDS
309 <222> LOCATION: (1)..(723)
312 <400> SEQUENCE: 3
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314 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
315 1          5          10          15
317 ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct      96
318 Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
319          20          25          30
321 gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt      144
322 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
323          35          40          45
325 gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag      192
326 Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
327          50          55          60
329 aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg      240
330 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
331 65          70          75          80
333 gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat      288

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RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9,10,11,12,13,14,15,16,17,18,23,24,25,26,27,28,29,30,31

VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date